

GENCORE version 4.3
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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	82	8.6	1188	2	A71621	protein with 5'-3'
2	79.5	8.4	665	2	T18979	hypothetical prote
3	79.5	8.4	851	2	T51545	receptor protein k
4	78	8.2	564	2	S73405	hexosephosphate tr
5	77.5	8.1	352	2	D82442	probable peptide A
6	77.5	8.1	880	2	S49637	regulatory protein
7	77	8.1	326	1	VGXROS	glycoprotein VP7 p
8	77	8.1	326	1	VGXRHU	glycoprotein VP7 p
9	77	8.1	326	1	VGXRRH	glycoprotein VP7 p
10	76.5	8.0	233	2	S11688	tumor necrosis fac
11	76	8.0	525	2	E70125	hypothetical prote
12	75.5	7.9	222	2	T14847	MADS-box protein d
13	75.5	7.9	314	2	I50811	MHC class I protei
14	75.5	7.9	686	2	T20898	hypothetical prote
15	75	7.9	129	2	B35216	Fb14 protein - fow
16	75	7.9	575	2	T28230	ORF MSV069 probabl
17	74.5	7.8	233	1	S22052	tumor necrosis fac
18	74.5	7.8	355	2	D48976	Grp-binding regula
19	74.5	7.8	461	2	T41511	probable dolichol
20	74.5	7.8	475	2	S28476	rflB protein VC024
21	74.5	7.8	543	2	S68467	CD40 receptor-asso
22	74	7.8	567	2	I49272	CD40 receptor-asso
23	74	7.8	568	2	A55649	TNFR-associated pr
24	74	7.8	568	2	A55960	CD40 receptor-asso
25	73.5	7.7	345	2	E71858	hypothetical prote
26	73.5	7.7	504	2	T47446	hypothetical prote
27	73.5	7.7	609	1	A43458	replication protei
28	73	7.7	166	2	S12723	interferon gamma p
29	73	7.7	326	1	VGXR2S	glycoprotein VP7 p

10

RESULT 4

Db 61 GAWYM-----PIVORYSE-----TQFG-----GEFTEDAYTD--PYVSLIEKQSI 101

RESULT: 9
VGARHU
glycoprotein VP7 precursor - human rotavirus A
N:Alternate names: outer capsid protein VP7
C:Species: human rotavirus A
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C:Accession: G27620; A93520; A04134

R.Green, K.Y.; Midthun, K.; Gorziglia, M.; Hoshino, Y.; Kapikian, A.Z.; Chanock, R.M.; Virology 163, 153-159, 1987
 A:Title: Comparison of the amino acid sequences of the major neutralization protein of
 A:Reference number: A27620; MUID:88044489
 A:Accession: G27620
 A:Molecule type: genomic RNA
 A:Residues: 1-326 <GRE>
 A:Experimental source: serotype 2 strain HU5
 R:Dyall-Smith, M.L.; Holmes, I.H. Nucleic Acids Res. 12, 3973-3982, 1984
 A:Title: Sequence homology between human and animal rotavirus serotype-specific glycoprotein
 A:Reference number: A93520; MUID:84221410
 A:Accession: A93520
 A:Molecule type: DNA
 A:Residues: 1-326 <DYA>
 A:Cross-references: GB:X00572; NID:g61680; PIDN:CAA25236.1; PID:g61681
 A:Experimental source: serotype 2 strain Hu/Australia/5/7
 C:Genetics:
 C:Map position: segment 9
 C:Superfamily: rotavirus glycoprotein VP7
 C:Keywords: coat protein; glycoprotein; transmembrane protein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-326/Product: glycoprotein VP7 #status predicted <GPV>
 F:32-48/Region: hydrophobic #status predicted
 F:69,146,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.1%; Score 77; DB 1; Length 326;
 Best Local Similarity 22.8%; Pred. No. 7.4;
 Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;
 QY 26 LWFCSIVMLFLFC-----SFWMLFIFLOLETAKEPCMAK-----RGPLPSKWMQ 71
 Db 10 LTLISILLNLIKLTITMIDYIFRLLILALISPPVQTQNGYGMWLPITGSLDAVYTN 69
 QY 72 ASSEPP-----CV-----NKVSDWKLEILQNGLYLIYQVAPNA---NYNDVAPVEV 115
 Db 70 STSGEPFLSTLCILYPAEAKNEISDEWENTLSQFLTKWPGISVYFKDYNIDNTFSV 129
 QY 116 --RLYKNKMIOTLTNKSQIONVGTGYELHVGDTIDLFNSEHOVLKNYWGIIILANP 173
 Db 130 NPQLYCDYNNV-----LMRYDNTSELDASELADILNE-----W-----LCNP 167
 QY 174 QFIS 177
 Db 168 MDIS 171

RESULT 10
 S11688
 tumor necrosis factor alpha precursor - cat
 C:Species: Felis silvestris catus (domestic cat)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
 C:Accession: S11688
 R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A. Nucleic Acids Res. 18, 5563, 1990
 A:Title: Gene sequence of feline tumor necrosis factor alpha.
 A:Reference number: S11688; MUID:91016860
 A:Accession: S11688
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <MCG>
 A:Cross-references: EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777
 C:Genetics:
 A:Introns: 62/3; 78/1; 94/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
 F:19,20/Binding site: myristate (lys) (covalent) #status predicted
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:145-177/Disulfide bonds: #status predicted

Query Match 8.0%; Score 76.5; DB 2; Length 233;

Best Local Similarity 20.2%; Pred. No. 5.6;
 Matches 50; Conservative 31; Mismatches 54; Indels 113; Gaps 12;
 QY 7 ENMPLSHSRTOGAQRSGSWKWLWLFCSIVMLLFLCSFSLIF-----IFLOLETAKEPCMAK 61
 Db 15 EALPKKAGGPOGSGR-----CLCLSLFSLVAGATTILF-----CLLH 52
 QY 62 FG-----PLPSKWOMAS-----SEPPCVN----- 80
 Db 53 FGVIQPRELPHGLQILNPLPOTLRSSSRTPSKPVAHVANPEAGLOLRSRANAL 112
 QY 81 -----KVSDWKLEILQNGLYLIYQV-----APNANY-----NDVAPFEVRLYKKNKDMT 126
 Db 113 LANGVELTNDOLKVPDGLYLIYQVLFVGGQCPSTHLLTHAISRFAYSVQTKNLLISA 172
 QY 127 LTNKSKIQN-----VGGTYELHVGDTID-----LIENSEHOVLKNN 162
 Db 173 I--KSPQRETPEGAEAKPWYEPYILGGVQLEKGRDRLSTEINLPAYLDFAESGV----- 226
 QY 163 TYWGIILL 170
 Db 227 -YFGIILAL 233

RESULT 11
 E70125
 hypothetical protein BB0205 - Lyme disease spirochete
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)
 C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
 C:Accession: E70125
 R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
 Bowman, C.; Garland, S.; Fujii, C.; Coton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A:Authors: Smith, H.O.; Venter, J.C.
 A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
 A:Reference number: A70100; MUID:98065943
 A:Accession: E70125
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Residues: 1-525 <KLE>
 A:Molecule type: DNA
 A:Cross-references: GB:AE001131; GB:AE000783; NID:g2688098; PIDN:AAC66601.1; PID:g268
 A:Experimental source: strain B31
 C:Superfamily: Borrelia burgdorferi hypothetical protein BB0205

Query Match 8.0%; Score 76; DB 2; Length 525;
 Best Local Similarity 23.1%; Pred. No. 16;
 Matches 37; Conservative 28; Mismatches 53; Indels 42; Gaps 7;
 QY 44 LIFTFLOLETAKE---PCMAKFGPLP-----SKWOMASSEPPCVNKSVDKMLEI 89
 Db 345 LVRFICIVDYDELVNPFIKESANPLETVKFLIENSGKYWSRKEPQCTKNKFFDIKM 404
 QY 90 LONGLYLI-----YQVAP-----NANYNDVAPFEVRL-----YKNKDMI 124
 Db 405 LENLFTILAPFDYGGQIVDVNKNKNENLFOAAVLEYKMSIAFNLSINKKNQTYKEEII 464
 QY 125 QTLTKNS-KIONVGGTYELHVGDTID--LIENSEHOVLKN 161
 Db 465 MDLENKEILIKDANGYKKNPLNNVDDFVINKSIPELKNK 504

RESULT 12
 T14847
 MAUS-box protein dal2 - Norway spruce
 C:Species: Picea abies (Norway spruce)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
 C:Accession: T14847
 R:Tandre, K.; Albert, V.A.; Sundas, A.; Engstrom, P.
 Plant Mol. Biol. 27, 69-78, 1995
 A:Title: Conifer homologues to genes that control floral development in angiosperms.
 A:Reference number: S51934; MUID:95170009

A:Accession: T14847
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-222 <TAN>
A:Cross-references: EMBL:X79280; NID:g695687; PIDN:CAA55867.1; PID:g695688
A:Experimental source: female cone
C:Genetics:
A:Gene: dal2
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 7.9%; Score 75.5; DB 2; Length 222;
Best Local Similarity 20.0%; Pred. No. 6.5;
Matches 32; Conservative 32; Mismatches 65; Indels 31; Gaps 5;

QY 15 RTGAGRSKWLFCISIVMLLFCFSWLIFFIFLQ-----LETAKEPCM-AKFGPLPS 67
DB 24 RNLGLKAYELSVLCDAEVALIVFSSRGLYEFANHSVKRTIERYKKTCDVNNHGGVIS 83
QY 68 K-----WOMASSEPCVKNKVDKLEILONGLYLYGOVAPNANNDVAPFVRLYKNKD 122
DB 84 ESNQVWQCEAGK-----LRQIEILQANRHLMDGLTALNIKELKQLEVRLEKIG 136
QY 123 MIOTLNKSKIONGVGYELHVGDTIDLFNSEHOVLKNN 162
DB 137 RVRSKKNEMLLEF-----IDIMORREHILIQEN 164

RESULT 13
I50811
MHC class I protein, alpha 1, alpha 2, alpha 3 and transmembrane domains - coelacanth (f
C:Species: Latimeria chalumnae (coelacanth)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 03-Dec-1999
C:Accession: I50811
R:Betz, U.A.K.; Mayer, W.E.; Klein, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 11065-11069, 1994
A:Title: Major histocompatibility complex class I genes of the coelacanth Latimeria cha
A:Reference number: I50810; MUID:95062206
A:Accession: I50811
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-314 <BET>
A:Cross-references: EMBL:U08034; NID:g549857; PIDN:AAA52346.1; PID:g560544
C:Genetics:
A:Gene: Lach-UB-01
A:Introns: 9/1; 183/1; 276/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 7.9%; Score 75.5; DB 2; Length 314;
Best Local Similarity 34.2%; Pred. No. 9.9;
Matches 26; Conservative 9; Mismatches 26; Indels 15; Gaps 5;

QY 55 KPCMAKFGPLPSKWMASSEPCVKNKVDKLEILONGLYLYGOVAPNANNDVAP 112
DB 138 KAOIRSKVCPVDEAMDSVFE-----DWKQECIE-GLKKYLLYGR---ETLERKVAP 185
QY 113 FEVRLYKNKDMIOQLT 128
DB 186 -EVRYDRPDLERNLT 200

RESULT 14
T20898
hypochemical protein F14F3.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20898
R:Kershaw, J.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19343

A:Accession: T20898
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-686 <WLL>
A:Cross-references: EMBL:Z49937; PIDN:CAA90184.1; GSPDB:CN00028; CESP:F14F3.2
A:Experimental source: clone F14F3
C:Genetics:
A:Gene: CESP:F14F3.2
A:Map position: X
A:Introns: 9/1; 49/1; 76/2; 100/2; 151/2; 212/3; 314/3; 380/2; 447/2; 508/2; 622/3; 6

Query Match 7.9%; Score 75.5; DB 2; Length 686;
Best Local Similarity 22.6%; Pred. No. 25;
Matches 40; Conservative 26; Mismatches 64; Indels 47; Gaps 6;

QY 11 LSHSRTOGAORSSWKLWLFCSIVMLLFCFSWLIFFIFLOLETAKEPCMAKFGPLPSKWQ 70
DB 319 MSAARNQRQR-----LAKFTPIQFIILLIDLIKDKRRITGDNPA--- 359
QY 71 MASSEPP-CVNKVDKLEILONGLYLYGOV-----PNANYN----- 108
DB 360 -PVSEPPKNRKSNDTPLRMKKSEVADYDEVAGISCSPTSGIVPNQANTLDESSRVW 418
QY 109 -DVAPFVRLYKNKDMIOQLTNKSKIONGVGYELHVGDTIDLFNSEHOVLKNNY 164
DB 419 DELLEMKERLSTETMTVVTLK-----QNEELTKLVHSLQAOINLINSELITFRDLY 471

RESULT 15
B35216
F14 protein - fowlpox virus (strain PP-1)
C:Species: fowlpox virus
C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 24-Nov-1999
C:Accession: B35216
R:Tartaglia, J.; Winslow, J.; Goebel, S.; Johnson, G.P.; Taylor, J.; Paoletti, E.
J. Gen. Virol. 71, 1517-1524, 1990
A:Title: Nucleotide sequence analysis of a 10.5 kbp HindIII fragment of fowlpox virus
A:Reference number: A35216; MUID:90324937
A:Accession: B35216
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <TAR>
A:Cross-references: GB:X17202; NID:g61222; PIDN:CAA35065.1; PID:g61225
C:Superfamily: fowlpox virus protein F14

Query Match 7.9%; Score 75; DB 2; Length 129;
Best Local Similarity 28.8%; Pred. No. 3.8;
Matches 23; Conservative 14; Mismatches 37; Indels 6; Gaps 3;

QY 31 STVMLLFLCSFSLWLIFFIFLOLETAKEPCMAKFGPLPSKWQ---ASSEPPCVNKVSKWKL 87
DB 6 SIYVLTWIGSCFYNPFI-LTYECRDDCCNGRYGVPVAPWPKVNLCTKIGGCCPD--SGYLL 62
QY 88 EILONGLYLYGOVAPNANY 107
DB 63 TTSENKTYCITGNETDKGY 82

Search completed: February 23, 2001, 10:49:52
Job time: 67 sec

